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Db      629 CT 630

RESULT 2
AU229698/c
LOCUS   AU229698
DEFINITION AU229698 RAF17 Arabidopsis thaliana cDNA clone RAF17-32-O17 3', mRNA sequence.
ACCESSION AU229698
VERSION   AU229698.1 GI:19798174
KEYWORDS  EST
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 438)
AUTHORS   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enyu,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE     Large scale analysis of Arabidopsis full-length cDNA
JOURNAL   Unpublished (2002)
COMMENT   Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4339
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda phage vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified phage vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.

FEATURES
source
1..438
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAF17-32-O17"
/lab_host="DH10B"
/clone_lib="RAF17"
/notes="Site 1: BamHI; Site 2: SalI; Subtraction Library.
The sequence was obtained from samples subjected to
dehydration-treated (1, 2, 5, 10 and 24 hr) and
rehydration-treated (1, 2, 5, 10, and 24 hr after
dehydration treatment)"

ORIGIN
Query Match 19.8%; Score 242; DB 9; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.1e-114; Indels 0; Gaps 0;
Matches 242; Conservative 0; Mismatches 0;

QY 819 AGGTTCTCTTAGGACCATAGGATGTGTTTGGCATCATCACTAGCTTCGTGT 878
Db |||||
405 AGGTTCTCTTAGGACCATAGGATGTGTTTGGCATCATCACTAGCTTCGTGT 346
QY |||||
879 TCTGATAGTCTCTCGGTGACTGAAGTTTCGCCGTGTTTTCGGGAGAA 938
Db |||||
345 TCTGATAGTCTCTCGGTGACTGAAGTTTCGCCGTGTTTTCGGGAGAA 286
QY |||||
939 GTTTTCAGGCAGAGAAAGGTGTCTCTCTACTCTTTCTCTTTGGGATTTCTCTTACTT 998
Db |||||
285 GTTTTCAGGCAGAGAAAGGTGTCTCTCTACTCTTTCTCTTTGGGATTTCTCTTACTT 226
QY |||||
999 CTACGGCGAGTTTAAATCCGGCAGAAAGTTGTGTGATAAACCTCAACCCGGCAGACAG 1058
Db |||||
225 CTACGGCGAGTTTAAATCCGGCAGAAAGTTGTGTGATAAACCTCAACCCGGCAGACAG 166

QY 1059 AC 1060
Db ||
165 AC 164

RESULT 3
H76984
LOCUS   H76984
DEFINITION H76984 Lambda-PRL2 Arabidopsis thaliana cDNA clone 200N2T7, mRNA sequence.
ACCESSION H76984
VERSION   H76984.1 GI:1054235
KEYWORDS  EST
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 589)
AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Rezel,E. and Somerville,C.
TITLE     Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL   Plant Physiol. 106, 1241-1255 (1994)
MEDLINE   95148729
PUBMED    7846151
COMMENT   Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcneibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
1..589
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="var Columbia"
/db_xref="taxon:3702"
/clone="200N2T7"
/clone_lib="Lambda-PRL2"
/notes="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."

ORIGIN
Query Match 14.3%; Score 175; DB 14; Length 589;
Best Local Similarity 99.6%; Pred. No. 2e-79;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 ATTATCCTCCTATAGGACATGGAGTCCCTTTGTTAACTGCTCTCTCTTCCACCAAT 114
Db |||||
1 ATTATCCTCCTATAGGACATGGAGTCCCTTTGTTAACTGCTCTCTCTTCCACCAAT 60
QY |||||
115 GCGGAAACCAATCTGTTTCATGAGTTCTCTATCAACCGCTGTTTCCAATCATCTC 174
Db |||||
61 GCGGAAACCAATCTGTTTCATGAGTTCTCTATCAACCGCTGTTTCCAATCATCTC 120
QY |||||
175 ATCCCTCTCTGGTCTCTTCTCCTCAGCGCTCGCGCAACCGCAACCTTACACGCG 234
Db |||||
121 ATCCCTCTCTGGTCTCTTCTCCTCAGCGCTCGCGCAACCGCAACCTTACACGCG 180
QY |||||
235 GAAACCAACGCGGAAACCAAGCTCTTCTCTATGGAAGCTCTCTCTGT 280

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Db 181 GAAACAAGCGAAGCAAGCTTCTCTCATGAACTCTCTGT 226
|||||

RESULT 4
BZ501737/C
LOCUS
DEFINITION BOMPA70TF BO.1.6.2_KB_tot Brassica oleracea genomic clone BOMPA70, GSS 15-DEC-2002
genomic survey sequence.
ACCESSION BZ501737
VERSION BZ501737.1 GI:27018757
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 807)
TOWN, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOMPA70TF
CONTACT: Chris Town
TIGR Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source
1..807
Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMPA70"
/clone_lib="BO.1.6.2_KB_tot"
/note="Vector: pHOSt1; Site: 1. BstXI; 1.6-2 kb sheared total DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN
Query Match 3.1%; Score 38; DB 28; Length 807;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 928 TTCGGGAGAGTTTCAGGAGAGAGGTGTCTCT 965
Db 797 TTCGGGAGAGTTTCAGGAGAGAGGTGTCTCT 760
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RESULT 5
CC457536
LOCUS
DEFINITION SALK_110605.26.10.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_110605.26.10.x, genomic survey sequence.
ACCESSION CC457536
VERSION CC457536.1 GI:31219753
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 395)
ALONSO, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)

FEATURES
source
1..784
Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHJF33"
/clone_lib="BOHJ"
/note="Vector: pHOSt1; Site: 1. BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt1 using BstXI linkers"

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atg28230.
Class: TDNA tagged.

FEATURES

source
1..395
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_110605.26.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 3.0%; Score 37; DB 28; Length 395;
Best Local Similarity 100.0%; Pred. NO. 1.6e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1007 AGTTTAATCCGCGAAGAGTTGTGATAAACCTCA 1043
Db 116 AGTTTAATCCGCGAAGAGTTGTGATAAACCTCA 152
|||||

RESULT 6

BH601144
LOCUS
DEFINITION BOHJF33TF BOHJ Brassica oleracea genomic clone BOHJF33, genomic survey sequence.
ACCESSION BH601144
VERSION BH601144.1 GI:17853590
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 784)
TOWN, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHJF33TR
CONTACT: Chris Town

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..784

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHJF33"

/clone_lib="BOHJ"

/note="Vector: pHOSt1; Site: 1. BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt1 using BstXI linkers"

ORIGIN